

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 16, 2002, 11:42:35 ; Search time 1709.23 Seconds  
(without alignments)  
2155.748 Million cell updates/sec

Title: US-09-761-579-2\_COPY\_1200\_1472

Perfect score: 273  
Sequence: 1 ctaccacatctactccagcg.....agatgaattattgagtgctt 273

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674877542 residues

al number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estha:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hic:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_hic:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrt:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	273	100.0	413	9	AA102428 zn24e05.s
C 2	273	100.0	424	9	AI306649 gn36p02.x
C 3	273	100.0	454	9	AA149954 zn03h02.s
C 4	273	100.0	456	9	AA639493 gn90c11.s
C 5	273	100.0	456	9	AI799955 wc41d03.x
C 6	273	100.0	463	9	BE222568 hu48b05.x
C 7	273	100.0	478	9	AA993771 ot65h04.s
C 8	273	100.0	484	9	AI493781 qz93d05.x
C 9	273	100.0	485	9	AA614036 no82c07.s
C 10	273	100.0	495	9	AI283292 qu13f08.x
C 11	273	100.0	497	9	AA687297 dv61b08.s
C 12	273	100.0	503	9	AA847355 oe82c07.s
C 13	273	100.0	512	9	AI313205 qz87b02.x
C 14	273	100.0	519	10	BB672988 7d26c06.x
C 15	273	100.0	537	9	AI459848 ar82h11.x
C 16	273	100.0	539	9	AI185025 qz35a06.s
C 17	273	100.0	565	9	AA552122 nk05g08.s

RESULT 1  
AA102428/c  
LOCUS  
DEFINITION  
z24e05.s1 Strategene neuroepithelium NTRAMI 937234 Homo sapiens  
CDNA clone IMAGE:548384 3' similar to gb:U3318 PYGVATE  
DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT, SOMATIC (HUMAN);, mRNA  
sequence.  
ACCESSION  
AA102428  
VERSION  
AA102428.1  
KEYWORDS  
EST.  
SOURCE  
human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 413)  
AUTHORS  
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,  
Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,  
M., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,  
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,  
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.  
Generation and analysis of 280,000 human expressed sequence tags  
Genome Res. 6 (9), 807-828 (1996)  
CONTACT: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
WARNING: There is evidence that suggests that the 384-well parent  
plate of this clone contains both human and mouse derived clones.  
Thus, the origin of this clone is uncertain. This caution should be  
kept in mind should you use this clone.  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Seq primer: -40M3 fwd. from Amersham  
High quality sequence stop: 331.  
Location/Qualifiers

## ALIGNMENTS

RESULT 1

AA102428/c

LOCUS

DEFINITION

z24e05.s1 Strategene neuroepithelium NTRAMI 937234 Homo sapiens

CDNA clone IMAGE:548384 3' similar to gb:U3318 PYGVATE

DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT, SOMATIC (HUMAN);, mRNA

sequence.

ACCESSION

AA102428

VERSION

AA102428.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 413)

AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,

M., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,

Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevaskis, E.,

Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.

Generation and analysis of 280,000 human expressed sequence tags

Genome Res. 6 (9), 807-828 (1996)

CONTACT: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@wustl.edu

WARNING: There is evidence that suggests that the 384-well parent

plate of this clone contains both human and mouse derived clones.

Thus, the origin of this clone is uncertain. This caution should be

kept in mind should you use this clone.

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Seq primer: -40M3 fwd. from Amersham

High quality sequence stop: 331.

Location/Qualifiers

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source
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/db_xref="GDB:3926900"
/db_xref="taxon:9606"
/clone="IMAGE:548384"
/clone_lib="Stratagene neuroepithelium NT2RAMI 937234"
/dev_stage="Ntera-2/RAMi neuroepithelial cells"
/label="Ntera-2/RAMi (kanamycin resistant)"
/notes="Vector: phuescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. NT2 (Ntera-2/cl.D1) precursor cells induced with Retinoic Acid for 1 week, followed by 3 weeks in mitotic inhibitors (replate 12). Average insert size: 1.1 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTT 3'."
BASE COUNT 105 a 108 c 71 g 125 t
ORIGIN
Query Match 100.0%; Score 273; DB 9; Length 413;
est Local Similarity 100.0%; Pred. No. 1e-67;
atches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctaccacatctactcagcagccaccctttgaagttcgtgtgccaatcagtgatcaa 60
Db 281 CTACCACATCTACTCCAGCGCCACCCTTTGAAGTTCTGTTGCGCCANTCAGTGGATCAA 222
Qy 61 gtttaagtcagtcagtttaaggaggaggaaggaggttatcccttcaggggggtaccag 120
Db 221 GTTTAAGTCAGTCAGTTAAGGGGAGGAGAGAGGTTATACCTTTCAGGGGGCTACCAG 162
Qy 121 acaggttctcaactgttgaaggaggagaagaaacccagtcgaatgaattcaatgaatt 180
Db 161 ACAGTGTCTCAACTGTGTTAAGGAGGAGAGAAACCCAGTCAGTGAATTCAGTGAATTT 102
Qy 181 ctggaaacctccattgaagtgtagattgagcaggttagtaattgcagtcagtttgataca 240
Db 101 CTGGAAACTTCATTAAGTGTGATAGTTCAGCAGGTAGTAAATTCATGTCAGTTTGATA 42
Qy 241 ttatgcattaaagaatgaattatgagtcgtt 273
Db 41 TTATGTCATTAAGAGATGAATTTATGAGTGCTT 9

RESULT 2
AI306649/c
LOCUS
DEFINITION
q38602.x1 NCI_CGAP_kid5 Homo sapiens cDNA clone IMAGE:1900299 3'
similar to gb:L13318 PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA
SUBUNIT, SOMATIC (HUMAN);, mRNA sequence.
AI306649
AI306649.1 GI:3989720
EST.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 424)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/dbbrp/image/image.html
Insert Length: 588 Std Error: 0.00

Seq primer: -40UP from Gibco
High quality sequence stop: 392.
Location/Qualifiers
source
1. .424
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1900299"
/clone_lib="NCI_CGAP_kid5"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/notes="Organ: kidney; Vector: p7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dt) primer [5',
AATGAGAGATTCGGCGCGCAATATTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo. "
```

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BASE COUNT 107 a 115 c 72 g 130 t
ORIGIN
Query Match 100.0%; Score 273; DB 9; Length 424;
Best Local Similarity 100.0%; Pred. No. 1e-67;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctaccacatctactcagcagccaccctttgaagttcgtgtgccaatcagtgatcaa 60
Db 283 CTACCACATCTACTCCAGCGCCACCCTTTGAAGTTCTGTTGCGCCANTCAGTGGATCAA 224
Qy 61 gtttaagtcagtcagtttaaggaggaggaaggaggttatcccttcaggggggtaccag 120
Db 223 GTTTAAGTCAGTCAGTTAAGGGGAGGAGAGAGGTTATACCTTTCAGGGGGCTACCAG 164
Qy 121 acaggttctcaactgttgaaggaggagaagaaacccagtcgaatgaattcaatgaatt 180
Db 163 ACAGTGTCTCAACTGTGTTAAGGAGGAGAGAAACCCAGTCAGTGAATTCAGTGAATTT 104
Qy 181 ctggaaacctccattgaagtgtagattgagcaggttagtaattgcagtcagtttgataca 240
Db 103 CTGGAAACTTCATTAAGTGTGATAGTTCAGCAGGTAGTAAATTCATGTCAGTTTGATA 44
Qy 241 ttatgcattaaagaatgaattatgagtcgtt 273
Db 43 TTATGTCATTAAGAGATGAATTTATGAGTGCTT 11

RESULT 3
AA149954/c
LOCUS
DEFINITION
z003h02.s1 Stratagene colon (#937204) Homo sapiens cDNA clone
IMAGE:566643 3' similar to gb:L13318 PYRUVATE DEHYDROGENASE E1
COMPONENT, ALPHA SUBUNIT, SOMATIC (HUMAN);, mRNA sequence.
AA149954
AA149954.1 GI:1721168
EST.
SOURCE
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 454)
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chisoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins
, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore
, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, K.,
Schellenberg, K., Soares, M.B., Tan, F., Thierry-Mieg, J., Trevas, E.,
Underwood, K., Wohlmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
9704478
JOURNAL
MEDLINE
COMMENT
Contact: Wilson RK
Washington University School of Medicine
```



JOURNAL  
COMMENT

Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: ccapbs@email.nih.gov  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmerit-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/bbrp/image/image.html  
Insert length: 606 Std Error: 0.00  
Seq primer: -40UP from Gibco.  
Location/Qualifiers

FEATURES  
source

1. .456  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2321189"  
/clone\_lib="NCI\_CGAP\_Pr28"  
/sex="male"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI\_CGAP\_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 112 a 120 c 75 g 149 t  
ORIGIN

Query Match 100.0%; Score 273; DB 9; Length 456;  
Best Local Similarity 100.0%; Pred. No. 1.1e-67;  
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctaccacatctctcagcagccacccttttgaattcgttggtgccaatcagtgatcaa 60  
DB 287 CTACCACATCTACTCCAGCGACCCACCTTTTGAAGTTCGTGTCCTCAATCAGTGATCAA 228  
QY 61 gtttaagtcagtcagttaaaggagagagagaggttatcacctcagggggtaccag 120  
DB 227 GTTTAAGTCAGTCAGTTAAGGGAGGAGAGAGAGGTTATACCTTCAGGGGGTACCAG 168  
QY 121 acagtgcttcactggttaaggagagagagagagagagagagagagagagagagag 180  
167 ACAGTGTCTCACTTGTTAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 108  
QY 181 ctggaaacttcattagtgtagagcagagtagtaattgcatgagttgataaatt 240  
DB 107 CTGGAAACTTCATTAAAGTGTGTAGATTGACGAGGTAGTAATTGCATGCTGTTGTACA 48  
QY 241 ttatgcatcattaaagataattattgagtgctt 273  
DB 47 TTATGTCATTAAAGATGAATATTAGTGCTT 15

## RESULT 6

BE222568/hu48b05.x1 NCI\_CGAP\_Pr241 Homo sapiens cDNA clone IMAGE:3173265 3', similar to gb:LI3318 PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT, SOMATIC (HUMAN));, mRNA sequence.  
LOCUS BE222568

ACCESSION BE222568  
VERSION BE222568.1 GI:8909886  
KEYWORDS EST.  
SOURCE human.

## ORGANISM

Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

## REFERENCE

1 (bases 1 to 463)  
NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BRGAP), Tumor Gene Index  
Unpublished (1998)  
Contact: Robert Strausberg, Ph.D.  
Email: ccapbs@email.nih.gov  
Tissue Procurement: Robert Jenkins, M.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D. and M. Fatima Bonaldo, Ph.D.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov  
Seq primer: -40UP from Gibco.  
Location/Qualifiers

FEATURES  
source

1. .463  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3173265"  
/clone\_lib="NCI\_CGAP\_Pr41"  
/tissue\_type="oligodendrogloma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: brain; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: NotI; Site 2: EcoRI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACCAATCTGAAGTGGAGCGGCGCATCTTTTCTTTTCTTTT 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library constructed and normalized by Bento Soares and M. Fatima Bonaldo."  
BASE COUNT 114 a 123 c 76 g 150 t  
ORIGIN

Query Match 100.0%; Score 273; DB 9; Length 463;  
Best Local Similarity 100.0%; Pred. No. 1.1e-67;  
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctaccacatctctcagcagccacccttttgaattcgttggtgccaatcagtgatcaa 60  
DB 282 CTACCACATCTACTCCAGCGACCCACCTTTTGAAGTTCGTGTCCTCAATCAGTGATCAA 223  
QY 61 gtttaagtcagtcagttaaaggagagagagagagagagagagagagagagagagag 120  
DB 222 GTTTAAGTCAGTCAGTTAAGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 163  
QY 121 acagtgcttcactggttaaggagagagagagagagagagagagagagagagagag 180  
DB 162 ACAGTGTCTCACTTGTTAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 103  
QY 181 ctggaaacttcattagtgtagagcagagtagtaattgcatgagttgataaatt 240  
DB 102 CTGGAAACTTCATTAAAGTGTGTAGATTGACGAGGTAGTAATTGCATGCTGTTGTACA 43  
QY 241 ttatgcatcattaaagataattattgagtgctt 273  
DB 42 TTATGTCATTAAAGATGAATATTAGTGCTT 10

## RESULT 7

AA993771/c

## LOCUS

## DEFINITION

AA993771

## ACCESSION

AA993771

## VERSION

AA993771.1

## KEYWORDS

EST.

## SOURCE

human.

AA993771  
ot65h04.s1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1621687  
3', similar to gb:LI3318 PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT, SOMATIC (HUMAN));, mRNA sequence.

AA993771

AA993771

AA993771.1

GI:3180316

EST.

human.

478 bp mRNA linear EST 27-AUG-1998  
Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1621687  
3', similar to gb:LI3318 PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT, SOMATIC (HUMAN));, mRNA sequence.

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ACCESSION      AI493781
VERSION        AI493781.1
KEYWORDS       GI:4394784
SOURCE         human
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE          1 (bases 1 to 484)
               NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
               National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
               Tumor Gene Index
               Unpublished (1997)
JOURNAL        Contact: Robert Strausberg, Ph.D.
COMMENT        Email: cgaps-remail.nih.gov
               This clone is available royalty-free through LNL : contact the
               IMAGE Consortium (info@image.llnl.gov) for further information.
               Insert Length: 543 Std Error: 0.00
               Seq primer: -400P from Gibco
               High quality sequence stop: 447.
               Location/Qualifiers
FEATURES       1..484
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               /db_xref="taxon:9606"
               /clone="IMAGE:2042121"
               /clone_lib="Soares_pregnant_uterus_NBHPU"
               /sex="female"
               /dev_stage="adult"
               /lab_host="DH10B"
               /note="Organ: uterus; Vector: pTT3-Pac; Site_1: Not I;
               Site_2: Eco RI; 1st strand cDNA was primed with a Not I
               oligo(dT) primer [5'
               AACTCGAAGAATTCGCGCGCCGCTTTTGTGTTTGTGTTT 3']
               double-stranded cDNA was ligated to Eco RI adaptors
               (Pharmacia), digested with Not I and cloned into the Not I
               and Eco RI sites of the modified pTT3 vector. Library
               went through one round of normalization. Library
               constructed by M. Fatima Bonaldo."
BASE COUNT    121 a 130 c 81 g 151 t 1 others
ORIGIN
Query Match      100.0%; Score 273; DB 9; Length 484;
Best Local Similarity 100.0%; Pred. No. 1.le-67;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctacacatctaccagcaccacaccttttgaagttcgtggtgcgaatcagtgatcaaa 60
|||||
DB 281 CTACACATCTACTCCAGCGACCCACCTTTTGAAGTTCTGTTGGTCCCAATCAGTGGATCAA 222
|||||
QY 61 gtttaagtcaagtcagtttaagggggaggagagagattatccttcaggggggtaccag 120
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DB 221 GTTTAAGTCAGTCAGTTAAGGGGAGGACAGAGAGAGGTTATACCTTCAGSGGGCTACCAAG 162
|||||
QY 121 acagttgtctcaacttggttaagggggaggaaaacccagtcgaatcgaattcaatgaatt 180
|||||
DB 161 ACAGTGTCTCAACTTGGTTAAGGAGGAGAAACCCAGTCATGAATTCATGAATTT 102
|||||
QY 181 ctctggaacttcattaaagtgtgaattgagcaggtagtaattgcagtcagttgttaca 240
|||||
DB 101 CTTGGAAACTTCCTAATTAAGTGTAGATTGACGAGGTAGTAATTGCATGCAGTTGTGACA 42
|||||
QY 241 ttagtgcattaaagaatgaattatgagctt 273
|||||
DB 41 TTAGTGCATTAAGAATGAATTAATTATGAGTGCTT 9
|||||
RESULT 9
AA614036/c AA614036 485 bp mRNA linear EST 18-FEB-1998
LOCUS      pos2c07.81 NCI-CGAP AA1 Homo sapiens cDNA clone IMAGE:111324 3'
DEFINITION similar to gb:U3318 PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA
SUBUNIT, SOMATIC (HUMAN);, mRNA sequence.
ACCESSION  AA614036

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Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 478)  
 NC1-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
 , Ph.D.  
 CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone Distribution: NC1-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
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 Seq primer: -40m13 fwd. ET from Amersham  
 High quality sequence stop: 362.  
 Location/Qualifiers  
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 /lab\_host="DH10B"  
 /note="vector: p773D-Pac (Pharmacia) with a modified  
 polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
 was prepared from mRNA obtained from Clontech Laboratories  
 , inc., and primed with a Not I - Oligo(dT) primer [5',  
 TGTTCACCAATCGAAGTGGAGGGCGGCCAATTTTTTTTTTTT 3'].  
 Double-stranded cDNA was ligated to Eco RI adaptors  
 (Pharmacia), digested with Not I and cloned into the Not I  
 and Eco RI sites of the modified p773 vector. Library  
 went through one round of normalization to Cot5, and was  
 constructed by Bento Soares and M. Fatima Bonaldo."  
 119 a 126 c 81 g 152 t  
 BASE COUNT  
 ORIGIN  
 Query Match 100.0%; Score 273; DB 9; Length 478;  
 Best Local Similarity 100.0%; Pred. No. 1.le-67;  
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ctacacatctactccagcaccaccccttttgagttcgtggtgccaatcagtgatcaa 60  
 |||||  
 283 CTACCAACATCTACTCCACGACCCACCCTTTTGAAGTTCGTGGTGGCAATCATGATCAA 224  
 |||||  
 QY 61 gtttaagtcagtcagttaaagggggaggagagaggttatccttcaggggggtaccag 120  
 |||||  
 DB 223 GTTTAAGTCAGTCAGTTAAGGGAGGAGAGAGAGGTTATACCTTCAGGGGGCTACCAG 164  
 |||||  
 QY 121 acagttcttccaacttgggttaaggagggaagaaacccagccaatgaattcaataaatt 180  
 |||||  
 QY 163 ACAGTGTCTCACTTGGTTAAGGAGGAGAAACCAGCAATGAATCAATGAATTT 104  
 |||||  
 DB 181 cttggaaacttcataaagtgtgagattgacagcaggtagtaattgcatgcagttgtaca 240  
 |||||  
 QY 103 CTTGGAAACTTCCATTAAAGTGTGTAGATTGACGAGGTAGTAATTGTCATGCAGTTGTGACA 44  
 |||||  
 DB 241 ttagtgcattaaaagatgaattattgagtgctt 273  
 |||||  
 DB 43 TTAGTGCAATTAAGATGAATTTATTGAGTGCTT 11  
 |||||  
 RESULT 8  
 AI493781/c 484 bp mRNA linear EST 18-MAR-1999  
 LOCUS  
 DEFINITION  
 IMAGE:2042121 3' similar to gb:U1318 PYRUVATE DEHYDROGENASE E1  
 COMPONENT, ALPHA SUBUNIT, SOMATIC (HUMAN);, mRNA sequence.

```

VERSION AA614036.1  GI:2466170
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 485)
JOURNAL NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
Ph.D.
cDNA Library Arraying: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert length: 1561 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 322.
Location/Qualifiers
1. .485
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI-CCAP_AAL"
/tissue_type="adrenal adenoma"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: adrenal gland; Vector: Bluescript SK-;
Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally.
Primer: Oligo dr. Two pooled bulk adrenal adenomas. 5'
adaptor sequence: 5' GAATTCGCCAGCAG 3' 3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3' Average insert
size: 1.6 kb."
123 a 129 c 83 g 150 t
BASE COUNT
ORIGIN

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Query Match	100.0%	Score 273;	DB 9;	Length 485;
Best Local Similarity	100.0%;	Pred. No. 1.1e-67;		
Matches 273;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ctaccacatctactccagcgaccacacttttgaagttcgtgggtgcgaatcagtggaatcaa	60	
	280	CTACACATCTACTCCAGCGACCACCTTTTGAAGTTCTGGTGGTCCCAATCAGTGGATCAA	221	
QY	61	gtttaagtcagtcagttaaaggggagagagagaggtataaccttcaggggggctaccag	120	
Db	220	GTTTAAGTCAGTCAGTTAAGGGGAGGAGAGAGAGGTTTACCTTTCAGGGGCTACCAG	161	
QY	121	acagtgttctcaacttggctaaaggagaaagaaacccagtcagatgaattcgaataaatt	180	
Db	160	ACAGTGTTCTCAACTTGGTTAAGGAGGAAGAAACCCAGTCAGTGAATTCAGTGAATTT	101	
QY	181	cttggaaccttcattgaagtgttagattagcgagggtagtaattgcatgctttgtaca	240	
Db	100	CTTGGNAACCTTCATTAAGTGTGTAGATTGAGCAGGTAGTAATTGTCATGCAGTTTGTACA	41	
QY	241	ttagtgcattaaaagatgaattattgagtgctt	273	
Db	40	TTAGTGCATTAAAGATCAATTAATTGAGTGCTT	8	

RESULT	10
AI283292/c	
LOCUS	A1283292
DEFINITION	ql3f08.x1 MCI.CGAP.Ov23 Homo sapiens cDNA clone IMAGE:1964679 3' similar to gb:L13318 PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA
	495 bp mRNA linear EST 23-NOV-1998

ACCESSION	Subunit, SOMATIC (HUMAN);, mRNA sequence.
VERSION	A1283292
KEYWORDS	A1283292.1 GI:3921525
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 495) NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)
JOURNAL	Contact: Robert Strausberg, Ph.D.
COMMENT	Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://www-bio.llnl.gov/bbrp/image/image.html">www-bio.llnl.gov/bbrp/image/image.html</a> Seq primer: -40UP from Gibco High quality sequence stop: 374. Location/Qualifiers 1. .495 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1964679" /clone_lib="NCI_CGAP_Ov23" /tissue_type="tumor, 5 pooled (see description)" /lab_host="DHL0B" /note="Organ: ovary; Vector: PCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.35 kb. Tumor types include: mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11534-013"
BASE COUNT	121 a 136 c 90 g 147 t 1 others
ORIGIN	

	Query Match	100.0%;	Score 273;	DB 9;	Length 495;	
	Best Local Similarity	100.0%;	Pred. No. 1.le-67;			
	Matches 273;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Oy	1	ctaccacatctactccagcaccacacotttttgaagttcgtgtggtgccaatcagttggatcaa	60			
Db	273	CTACCACATCTACTCCAGCAGCACCACCTTTTGAAGTTCGTGTGCCAATCAGTGGATCAA	214			
Oy	61	gtttaagtcagttcagtttaaaggggaggaagagaggtttatccttcaggggggtaccag	120			
Db	213	GTTTAAAGTCAGTCAGTTAAAGGGAGGAGAGAGGAGGTTATACCTTCAGGGGGCTACCA	154			
Oy	121	acagtggtcttcaacttggttcaaggaaggaagaaaccagtcgaatgaattcaatgaatt	180			
Db	153	ACAGTGTCTCAACTTGGTTAAGGAGGAGAAACCAGTCATGAATTCATATGAATTAAT	94			
Oy	181	cttggaaacttcattaaagtggttagattgagcaggtagtagtaattgcagcagttgttaca	240			
Db	93	CTTGGAAACHTCCATTAAGTGTGTAGATTGAGCAGGTAGTAATTCATGTCAGTTGTGACA	34			
Oy	241	ttagtgcaattaaagaatgaattattgagtctt	273			
Db	33	TTAGTGCATTAAAGAATGAATTTATTCAGTGCCTT	1			

RESULT	11
AA687297/C	
LOCUS	AA687297
DEFINITION	497 bp mRNA linear EST 24-DEC-1997 nv61b08.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1234263 3' similar to gb:U3318 PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA

Mon Aug 19 09:13:27 2002

similar to gb:U13318 PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT, SOMATIC (HUMAN);, mRNA sequence.

ACCESSION AA687297  
VERSION AA687297.1 GI:2675488  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 497)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index

JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov

unknown library type  
Insert Length: 800 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 441.  
Location/Qualifiers

1. 497  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="1234263"  
/clone\_lib="NCI-CGAP\_GCB1"  
/tissue\_type="germinal center B cell"  
/lab\_host="DH10B"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was prepared from human tonsillar cells enriched for germinal center B cells by flow sorting (CD20+, IgD-), provided by Dr. Louis M. Staudt (NCI). Dr. David Allman (NCI) and Dr. Gerald Marti (DBER). cDNA synthesis was primed with a Not I - oligo(dT) primer [5'-GTGACCAATCTGAAGTGGAGCGCCCTCATTTTTTTTTTTT-3' (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 118 a 129 c 81 g 169 t  
ORIGIN

Query Match 100.0%; Score 273; DB 9; Length 497;  
Best Local Similarity 100.0%; Pred. No. 1.1e-67;  
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/ 1 ctaccacatctactccagcaccaccccttttgaagttcgtggtgccaatcagtgatcaa 60  
Db 295 CTACCACATCTACTCCAGCGACCCACCTTTTGAAGTTCGTGTCGCAATCAGTGGATCAA 236  
QY 61 gtttaagtcagtcagtttaagggaggagagagaggttatccttcagggggctaccag 120  
Db 235 GTTTAAGTCAGTCAGTTAAGGGGAGGAGAGAGAGGTTATACCTTCAGGGGGTACCAG 176  
QY 121 acagtgcttcaacttggttaagggaggagaaacccagtcacatgaattcaatgaatt 180  
Db 175 ACAGTGTTCTCAACTTGGTTAAGGAGGAGAAACCCAGTCAATGAATTCATGAATTT 116  
QY 181 ctggaaacttcatttaagtggttagattgagcaggttagattgagcaggtttgtaca 240  
Db 115 CTTGGAACCTCCATTAAGTGTGTAGATTGAGCAGGTAGTATTGTCAGTCAGTTGTACA 56  
QY 241 ttagtgcattaaaagatgaattattagtgctt 273  
Db 55 TTAGTGCATTAAAGATGAATTTATTGAGTGCTT 23

RESULT 12  
AA847355 503 bp mRNA linear EST 31-WAR-1998  
LOCUS AA847355  
DEFINITION ce82c07.s1 NCI\_CGAP\_Col12 Homo sapiens cDNA clone IMAGE:1418124

ACCESSION AA847355  
VERSION AA847355.1 GI:2933873  
KEYWORDS EST.  
SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 503)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index

JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov

Emmert-Buck, M.D., Ph.D.  
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. CDNA Library Prepared by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www.bio.llnl.gov/bbrp/image/image.html  
Insert Length: 1140 Std Error: 0.00  
Seq primer: -40ml3 fwd. ET from Amersham  
High quality sequence stop: 290.  
Location/Qualifiers

1. 503  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="1418124"  
/clone\_lib="NCI\_CGAP\_Col12"  
/sex="mixed"  
/tissue\_type="colon tumor"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: colon; Vector: Bluescript SK-; Site 1: EcoRI  
; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo  
dT. Pooled colon tumors. 5' adaptor sequence: 5'  
GAATTCGGCAGCAG 3' 3' adaptor sequence: 5'  
CTCGAGTTTTTTTTTTTTTTT 3' Average insert size: 1.2 kb."

BASE COUNT 127 a 132 c 95 g 149 t  
ORIGIN

Query Match 100.0%; Score 273; DB 9; Length 503;  
Best Local Similarity 100.0%; Pred. No. 1.1e-67;  
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctaccacatctactccagcaccaccccttttgaagttcgtggtgccaatcagtgatcaa 60  
Db 281 CTACCACATCTACTCCAGCGACCCACCTTTTGAAGTTCGTGTCGCAATCAGTGGATCAA 222  
QY 61 gtttaagtcagtcagtttaagggaggagagaggttatccttcagggggctaccag 120  
Db 221 GTTTAAGTCAGTCAGTTAAGGGGAGGAGAGAGAGGTTATACCTTCAGGGGGTACCAG 162  
QY 121 acagtgcttcaacttggttaagggaggagaaacccagtcacatgaattcaatgaatt 180  
Db 161 ACAGTGTTCTCAACTTGGTTAAGGAGGAGAAACCCAGTCAATGAATTCATGAATTT 102  
QY 181 ctggaaacttcatttaagtggttagattgagcaggttagattgagcaggtttgtaca 240  
Db 101 CTTGGAACCTCCATTAAGTGTGTAGATTGAGCAGGTAGTATTGTCAGTCAGTTGTACA 42  
QY 241 ttagtgcattaaaagatgaattattagtgctt 273  
Db 41 TTAGTGCATTAAAGATGAATTTATTGAGTGCTT 9

RESULT 13  
AA847355/c AI313205/LOCUS AI313205  
DEFINITION ce82c07.s1 NCI\_CGAP\_Col12 Homo sapiens cDNA clone IMAGE:1418124



DEFINITION qp87b02.x1 Soares\_fetal\_lung\_NbHL19W Homo sapiens cDNA clone IMAGE:1929963 3' similar to gb:U3318 PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT, SOMATIC (HUMAN);, mRNA sequence.

ACCESSION A1313205

VERSION A1313205.1 GI:4018810

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 512)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
This clone is available royalty-free through LNL; contact the IMAGE Consortium ([infoimage.llnl.gov](http://infoimage.llnl.gov)) for further information.  
Insert Length: 855 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 382.  
Location/Qualifiers  
1..512  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1929963"  
/clone\_lib="Soares\_fetal\_lung\_NbHL19W"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTACCACTGAGTGGAGGCGCGCAATTTTGTGTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Fatima Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBHL19W."

FEATURES  
source

BASE COUNT 128 a 134 c 85 g 165 t

ORIGIN

Query Match 100.0%; Score 273; DB 9; Length 512;  
Best Local Similarity 100.0%; Pred. No. 1.le-67;  
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ctaccacatctactcagcgaccacccctttgaagtcgtgtgccaatcagtgatcaa 60

Db 303 CTACCAACATCTACTCAGCGACCCACCTTTTGAGTTCGTGTGCGCAATCAGTGGATCAA 244

QY 61 gtttaagtcagtcagtaaggaggagagagaggttatcaccttcagggggctaccag 120

Db 243 GTTTAAGTCAGTCAGTTAAGGGGAGGAGAGAGGTTATACCTTCAGGGGGCTACCAG 184

QY 121 acagtgttctcaactgtgtaaggaggagagaaacccagtcgaatgaattcaatgaatt 180

Db 183 ACAGTGTCTCAACTTGGTTAAGGAGGAGAGAAACCCAGTCGAATGAATGAATGAATTT 124

QY 181 ctgggaacttccattaaagtgtgagattgagcagtagtaattgcatgagttgtaca 240

Db 123 CTGGAACCTTCCATTAAGTGTGTAGATTGAGCAGGTAGTATTGTCATGCAGTTGTACA 64

QY 241 ttagtgcattaaagatgaattattgagtcgtt 273

Db 63 TTAGTGCATTAAGAATGAATTTATTGAGTGCTT 31

RESULT 14  
BE672988/c

--

LOCUS BE672988 519 bp mRNA linear EST 08-SEP-2000

DEFINITION 7d26c06.x1 NCI-CGAP\_Pr28 Homo sapiens cDNA clone IMAGE:3248362 3' similar to gb:U3318 PYRUVATE DEHYDROGENASE E1 COMPONENT, ALPHA SUBUNIT, SOMATIC (HUMAN);, mRNA sequence.

ACCESSION BE672988

VERSION BE672988.1 GI:10033529

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 519)

AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: [info@image.llnl.gov](mailto:info@image.llnl.gov)  
Seq primer: -40UP from Gibco  
High quality sequence stop: 460.  
Location/Qualifiers  
1..519  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3248362"  
/clone\_lib="NCI-CGAP\_Pr28"  
/sex="male"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI-CGAP\_Pr22 was prepared, and as circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonesIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo."

FEATURES  
source

BASE COUNT 128 a 137 c 91 g 163 t

ORIGIN

Query Match 100.0%; Score 273; DB 10; Length 519;  
Best Local Similarity 100.0%; Pred. No. 1.le-67;  
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctaccacatctactcagcgaccacccctttgaagtcgtgtgccaatcagtgatcaa 60

Db 282 CTACCAACATCTACTCAGCGACCCACCTTTTGAGTTCGTGTGCGCAATCAGTGGATCAA 223

QY 61 gtttaagtcagtcagtaaggaggagagagaggttatcaccttcagggggctaccag 120

Db 222 GTTTAAGTCAGTCAGTTAAGGGGAGGAGAGAGGTTATACCTTCAGGGGGCTACCAG 163

QY 121 acagtgttctcaactgtgtaaggaggagagaaacccagtcgaatgaattcaatgaatt 180

Db 162 ACAGTGTCTCAACTTGGTTAAGGAGGAGAGAAACCCAGTCATGAATGAATGAATTT 103

QY 181 ctgggaacttccattaaagtgtgtagattgagcagtagtaattgcatgagttgtaca 240

Db 102 CTGGAACCTTCCATTAAGTGTGTAGATTGAGCAGGTAGTAAATTCATGTCAGTTGTACA 43

QY 241 ttagtgcattaaagatgaattattgagtcgtt 273

Db 42 TTAGTGCATTAAGAATGAATTTATTGAGTGCTT 10



Search completed: August 16, 2002, 13:08:49  
Job time: 5174 sec

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Location/Qualifiers
1. 537
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="2151813"
/clone_lib="Barstead colon HPLRB7"
/sex="male"
/dev_stage="adult, age 25"
/lab_host="PH108 (phage resistant)"
/notes="Organ: colon; Vector: p7T3D-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoRI; Site_2: NotI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTAGACATCTGAATGGAGCGGCCCGCCCTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
[5', AATCTACTAGTAAT 3', and 5', AATTACTAGT 3'], digested
with Not I and cloned into the Not I and Eco RI sites of
the modified p7T3 vector. Library constructed by Bob
Barstead."

```

BASE COUNT	133 a	147 c	95 g	162 t	Barstead.
ORIGIN					
Query Match	100.0%	Score 273;	DB 9;	Length 537;	
Best Local Similarity	100.0%;	Pred. No. 1.1e-67;			
Matches 273;	Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ctaccacatctactccagcgaccacacctttgaagttcgtgtgcgaatcagtgatcaa	60		
Db	280	CTACCACATCTACTCCAGGACCCACTTTGAAGTTCGTGTGCCTCAATCAGTGGATCAA	221		
QY	61	gtttaagtccagtcagttaaagggggaggagaggttatcaccttcagggggctaccag	120		
Db	220	GTTTAAGTCAGTTCAGTTAAGGGGAGGAGAGGAGGTTTACCTTCAGGGGCTACCAG	161		
QY	121	acagttcttcaccttggttaagagaggaagaaacccagtcgaatgaattcaatgaatt	180		
Db	160	ACAGTGTTCCTCAACTTGGTTAAGGAGGAAGAAACCCAGTCAATGAATTCATGAATTT	101		
QY	181	cttggaaacttcacattaaagtgtagattgagcaggttagtaattgcctgcagtttgtaca	240		
Db	100	CTTTGGAACCTTCATTAAGTGTGTAGATTGACGAGGTAGTAATTGTCATGTCAGTTTGTACA	41		



[illegible]





us-09-761-579-2\_copy\_1200\_1472.rni

Mon Aug 19 09:13:25 2002

```

GENERAL INFORMATION:
APPLICANT: Palmer, Leslie M.
TITLE OF INVENTION: No. 6010881e1 ribg
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,456
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P50444-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1029 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-369-700-1

Query Match      11.0%; Score 30; DB 4; Length 1029;
Best Local Similarity 54.5%; Pred. No. 2.2;
Matches 60; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 139 ttaaggaggagaagaaacccagtcgaatgaattcaatgaattcttggaaactccattaa 198
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Db 656 ATCAGCAAAATTTATCAAGATGAATCAACACCAATTGGATATATACTGAA 705
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RESULT 10
US-08-553-436A-1/C
Sequence 1, Application US/08553436A
Patent No. 5866790
GENERAL INFORMATION:
APPLICANT: HESSE, Holger
TITLE OF INVENTION: DNA SEQUENCES AND PLASMIDS FOR THE
PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE
CONCENTRATION
TITLE OF INVENTION: PREPARATION OF SUGAR BEET WITH CHANGED SUCROSE
CONCENTRATION
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen
STREET: 1180 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,436A
FILING DATE: 17-NOV-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP94/01671
FILING DATE: 20-MAY-1994
PRIOR APPLICATION NUMBER: DE P 4317596.1
FILING DATE: 24-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weillman, Edward
REGISTRATION NUMBER: 24,735

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GENERAL INFORMATION:
APPLICANT: Palmer, Leslie M.
TITLE OF INVENTION: No. 6010881e1 ribg
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,456
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P50444-9
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
TELEFAX: 215-994-2222
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1029 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-978-456-1

Query Match      11.0%; Score 30; DB 3; Length 1029;
Best Local Similarity 54.5%; Pred. No. 2.2;
Matches 60; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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Db 656 ATCAGCAAAATTTATCAAGATGAATCAACACCAATTGGATATATACTGAA 705
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US-09-369-700-1
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Patent No. 6280735
GENERAL INFORMATION:
APPLICANT: Palmer, Leslie M.
TITLE OF INVENTION: No. 6280735e1 ribg
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: US
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

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RESULT 11
US-08-977-554-7
; Sequence 7, Application US/08977554
; Patent No. 5891672
; GENERAL INFORMATION:
; APPLICANT: Palmer, Leslie M.
; APPLICANT: Padner, Jason C.
; APPLICANT: Warren, Richard L.
; APPLICANT: Train, Christopher
; APPLICANT: Wang, Min
; APPLICANT: Jaworski, Deborah D.
; APPLICANT: Mooney, Jeffrey
; APPLICANT: Debouck, Christine
; APPLICANT: Zhong, Yiyi
; APPLICANT: Black, Michael
; TITLE OF INVENTION: r1ba
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert, Price & R...
; STREET: 4000 Bell Atlantic To...
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2793
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows...
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; APPLICATION NUMBER: US/08/977...
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/...
; FILING DATE: 19-FEB-1997

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; Sequence 7, Application US/08978456  
; Patent No. 6010881  
; GENERAL INFORMATION:  
; APPLICANT: Palmer, Leslie M.  
; TITLE OF INVENTION: No. 6010881el ribG  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Dechert Price & Rhoads  
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: US  
; ZIP: 19103  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
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; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/978,456  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dickinson, Todd O  
; REGISTRATION NUMBER: 28,354  
; REFERENCE/DOCKET NUMBER: P50444-9  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 215-994-2252  
; TELEFAX: 215-994-2222  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3336 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
US-08-978-456-7



400

**Gaps**      **0;**

198

TTA 655

Mon Aug 19 09:13:25 2002

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APPLICANT: Warren, Richard L.
APPLICANT: Traini, Christopher M.
APPLICANT: Wang, Min
APPLICANT: Jaworski, Deborah D.
APPLICANT: Mooney, Jeffrey
APPLICANT: Debouck, Christine
APPLICANT: Zhong, Yiyi
APPLICANT: Black, Michael
TITLE OF INVENTION: ribA
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert, Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/227,806
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/977,554
FILING DATE:
APPLICATION NUMBER: PCT/US97/02318
FILING DATE: 19-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dickinson, Q. Todd
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: P50444-07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215/994-2252
TELEFAX: 215/994-2222
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3336 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-227-806-7

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Query Match      11.0%; Score 30; DB 4; Length 3336;
est Local Similarity 54.5%; Pred. No. 3.4;
Matches 60; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

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Db 596 TTCAGATGGAAGAAACCCCTATAAAGTAAATATTGCTAAGTCTGGGAATATTCATTTA 655
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Db 656 ATCAGCAATTTATCAAGATGATCAACACCAATTTGGATATATATACTGAA 705
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Job time: 6726 sec

us-09-761-579-2-copy\_1200\_1472.rng

Mon Aug 19 09:13:24 2002

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 16, 2002, 12:35:24 ; Search time 211.74 Seconds  
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2213.647 Million cell updates/sec

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Scoring table: Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues 3472872  
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Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	215.4	78.9	275	22 AAL23550	Human breast cance
3	210.4	77.1	311	22 AAL14688	Human breast cance
4	34.6	12.7	7316	24 ABL32060	Human immune syste
5	33.8	12.4	27179	22 AAS34556	Human DNA for a no
6	33.6	12.3	113515	24 ABL34175	Human immune syste
7	33.2	12.2	2700	23 AAS65647	DNA encoding novel
8	33.2	12.2	3613	23 ABL16660	Drosophila melanog
9	33.2	12.2	4356	23 ABL16478	Drosophila melanog

10	32.6	11.9	1464	21 AAC48192	Arabidopsis thalia
11	32.6	11.9	18890	23 ABL13818	Drosophila melanog
12	31.8	11.6	878	21 AAC69616	Human secreted pro
13	31.8	11.6	6899	24 ABL33894	Human immune syste
14	31.6	11.6	394	18 AAT65070	Canine genomic mic
15	31.6	11.6	394	20 AAX17807	Microsatellite rep
16	31.6	11.6	2938	14 AAQ50644	Human Hum-Fil-1 ge
17	31.6	11.6	2954	22 AAH02915	Human shear stress
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19	31.2	11.4	8323	24 ABL32058	Human immune syste
20	31	11.4	3227	22 AAS03283	C. elegans cDNA en
21	31	11.4	3709	22 AAS03282	C. elegans genomic
22	31	11.4	1503900	22 AAK95240	Human neuregulin-1
23	31	11.4	1503900	22 AAK96733	Human neuregulin-1
24	30.8	11.3	3303	21 AAT70147	Plasmodium falcipa
25	30.8	11.3	63563	22 AAF28546	Genomic fragment #
26	30.6	11.2	240	22 AAI91712	Human polynucleoti
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28	30.6	11.2	3072	21 AAC47196	Arabidopsis thalia
29	30.6	11.2	3594	21 AAC50212	Arabidopsis thalia
30	30.6	11.2	6665	22 AAS45299	Chemically pretrea
31	30.6	11.2	6665	24 ABL32083	Human immune syste
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36	30.4	11.1	17142	24 ABL34107	Human immune syste
37	30.2	11.1	547	21 AAZ87243	Partial cDNA clone
38	30.2	11.1	695	21 AAZ87236	cDNA clone #2 enco
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40	30.2	11.1	3753	23 AAS68937	DNA encoding novel
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## ALIGNMENTS

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XX AAT21382;  
AC 01-AUG-1996 (first entry)  
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DE Gene signature; messenger RNA; mRNA; relative abundance; frequency;  
KW human; cloning; mapping; non-biased library; diagnosis; detection;  
KW cell typing; abnormal cell function; ss.  
XX Homo sapiens.  
XX WO9514772-Al.  
XX 01-JUN-1985.  
XX 11-NOV-1994; 94WO-JP01916.  
XX 12-NOV-1993; 93JP-0355504.  
XX (MATS/) MATSUBARA K.  
XX (OKUB/) OKUBO K.  
XX Matsubara K, Okubo K;  
XX WPI; 1995-206931/27.  
XX Identifying gene signatures in 3'-directed human cDNA library - e.g.  
PT





PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
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PR 07-JUL-2000; 2000US-0216647.  
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PR 11-JUL-2000; 2000US-0217487.  
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PR 26-JUL-2000; 2000US-0220963.  
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PR 20-OCT-2000; 2000US-0240960.  
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PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
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PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-488782/53.

New polynucleotides and polypeptides for diagnosing, treating,  
preventing or prognosising e.g. diseases or disorders of the nervous,  
musculoskeletal, excretory, gastrointestinal, reproductive, and

Mon Aug 19 09:13:24 2002

XX 30-JUN-2000; 2000DE-1032529.  
PR 01-SEP-2000; 2000DE-1043826.  
XX (EPIC-) EPIGENOMICS AG.  
XX Olek A, Piepenbrock C, Berlin K;  
XX WPI; 2002-130909/17.  
XX Nucleic acid comprising fragment of chemically modified gene, useful  
PT for diagnosis and treatment of diseases associated with abnormal  
PT cytosine methylation  
XX Claim 1; SEQ ID NO 2148; 32pp + Sequence Listing; German.  
XX The present invention provides a number of human immune system associated  
XX genes which are modified by the methylation of cytosines. The sequences  
XX can be used in the diagnosis and treatment of immune system disorders,  
XX including eye diseases such as retinopathy, neovascular glaucoma and  
XX macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
XX leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
XX rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel  
XX diseases. The present sequence is a gene of the invention.  
XX Sequence 113515 BP; 35172 A; 1174 C; 22520 G; 54649 T; 0 other;  
SQ  
Query Match 12.38; Score 33.6; DB 24; Length 113515;  
Best Local Similarity 50.0%; Pred. No. 7.6;  
Matches 84; Conservative 0; Mismatches 84; Indels 0; Gaps 0;  
QY 99 tatacttcagggggctaccagacagtggtctcaacttggttaaggaggagagaaaccca 158  
Db 10648 tttatatgtatgag 10707  
QY 159 gtcaatgaattcaatgaattcttggaaacttccatcaatgaattgtagtagcaggta 218  
Db 10708 aggaataaaag 10767  
QY 219 gtaattgcagtcagctgtgtacattagtcattataaagatgaattattg 266  
Db 10768 gggattaaatgggtttatttttttttttttttttttttttttttttttttttt 10815  
RESULT 7  
AAS65647/C  
ID AAS65647 standard; cDNA; 2700 BP.  
XX AC AAS65647;  
XX DT 13-FEB-2002 (first entry)  
XX DE DNA encoding novel human diagnostic protein #1451.  
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
XX NW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX OS Homo sapiens.  
XX PN WO200175067-A2.  
XX PD 11-OCT-2001.  
XX PF 30-MAR-2001; 2001WO-US08631.  
XX PR 31-MAR-2000; 2000US-0540217.  
XX PR 23-AUG-2000; 2000US-0649167.  
XX PA (HYSE-) HYSEQ INC.  
XX PI Drmanac RT, Liu C, Tang YT;  
XX

PT respiratory systems  
PS Disclosure; SEQ ID NO 1980; 642pp; English.  
XX The invention relates to novel nucleic acids encoding novel human foetal  
XX antigens. The nucleic acids and proteins are used to prevent, treat (e.g.  
XX by gene therapy) or ameliorate a medical condition in e.g. humans, mice,  
XX rabbits, goats, horses, cats, dogs, chickens or sheep. They  
XX are also used in diagnosing a pathological condition or susceptibility  
XX to a pathological condition. The antibodies to the antigens can also  
XX be used in alleviating symptoms associated with the disorders and in  
XX diagnostic immunoassays e.g. radioimmunoassays or enzyme linked  
XX immunosorbent assays (ELISA). Disorders which are diagnosed or treated  
XX include autoimmune diseases e.g. rheumatoid arthritis,  
XX hyperproliferative disorders e.g. neoplasms of the breast or liver,  
XX cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
XX e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.  
XX Alzheimer's disease, infections caused by bacteria, viruses and fungi  
XX and ocular disorders e.g. corneal infection. The polypeptides can also  
XX be used to aid wound healing and epithelial cell proliferation, to  
XX prevent skin aging due to sunburn, to maintain organs before  
XX transplantation, for supporting cell culture of primary tissues, to  
XX regenerate tissues and in chemotaxis. The polypeptides can also be used  
XX as a food additive or preservative to increase or decrease storage  
XX capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
XX minerals, cofactors and other nutritional components. Numerous  
XX examples of diseases and disorders treated by the nucleic acids and  
XX proteins are given in the specification. The present sequence  
XX is a genomic DNA fragment from a gene encoding a foetal antigen of the  
XX  
Query Match 12.48; Score 33.8; DB 22; Length 27179;  
Best Local Similarity 52.5%; Pred. No. 3.8;  
Matches 74; Conservative 0; Mismatches 67; Indels 0; Gaps 0;  
QY 125 tttctcaacttggttaaggaggagagagagagagagagagagagagagagagagagag 184  
Db 9159 tctctggaaatagtttagttagttagttagttagttagttagttagttagttagttag 9218  
QY 185 gaacttcattcaatgaattgtagagtagtagtagtagtagtagtagtagtagtagtagtag 244  
Db 9219 cacatttccttttagttagttagttagttagttagttagttagttagttagttagttag 9278  
QY 245 tgcattaaaaagatgaattatt 265  
Db 9279 ttcagtaaaaaagctttttatt 9299  
RESULT 6  
U34175  
ABL34175 standard; DNA; 113515 BP.  
XX AC ABL34175;  
XX DT 26-MAR-2002 (first entry)  
XX DE Human immune system associated gene SEQ ID NO: 2148.  
XX KW Human; immune system disease; cytosine methylation; antiasthmatic;  
XX NW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
XX KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;  
XX KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;  
XX KW acute myeloid leukemia; Alzheimer's disease; AIDS; epilepsy;  
XX KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;  
XX KW gene; ds.  
XX OS Homo sapiens.  
XX PN WO200200928-A2.  
XX PD 03-JAN-2002.  
XX PR 02-JUL-2001; 2001WO-EP07537.  
XX





[illegible]

PR	22-JUL-1999;	99US-0145085.
PR	22-JUL-1999;	99US-0145087.
PR	22-JUL-1999;	99US-0145089.
PR	22-JUL-1999;	99US-0145192.
PR	23-JUL-1999;	99US-0145145.
PR	23-JUL-1999;	99US-0145218.
PR	23-JUL-1999;	99US-0145224.
PR	26-JUL-1999;	99US-0145276.
PR	27-JUL-1999;	99US-0145913.
PR	27-JUL-1999;	99US-0145918.
PR	27-JUL-1999;	99US-0145919.
PR	28-JUL-1999;	99US-0145951.
PR	28-JUL-1999;	99US-0146386.
PR	02-AUG-1999;	99US-0146388.
PR	02-AUG-1999;	99US-0146389.
PR	02-AUG-1999;	99US-0147038.
PR	03-AUG-1999;	99US-0147204.
PR	04-AUG-1999;	99US-0147302.
PR	04-AUG-1999;	99US-0147192.
PR	05-AUG-1999;	99US-0147260.
PR	05-AUG-1999;	99US-0147303.
PR	06-AUG-1999;	99US-0147416.
PR	06-AUG-1999;	99US-0147493.
PR	09-AUG-1999;	99US-0147935.
PR	09-AUG-1999;	99US-0148171.
PR	10-AUG-1999;	99US-0148319.
PR	11-AUG-1999;	99US-0148341.
PR	12-AUG-1999;	99US-0148565.
PR	13-AUG-1999;	99US-0148664.
PR	13-AUG-1999;	99US-0149368.
PR	16-AUG-1999;	99US-0149375.
PR	17-AUG-1999;	99US-0149426.
PR	18-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149930.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150894.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	27-AUG-1999;	99US-0151303.
PR	30-AUG-1999;	99US-0151438.
PR	31-AUG-1999;	99US-0151930.
PR	01-SEP-1999;	99US-0152363.
PR	07-SEP-1999;	99US-0153070.
PR	10-SEP-1999;	99US-0153758.
PR	13-SEP-1999;	99US-0154018.
PR	15-SEP-1999;	99US-0154039.
PR	16-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155639.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159658.
PR	18-OCT-1999;	99US-0159564.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.



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XX PS Claim 1; SEQ ID NO 1867; 32pp + Sequence Listing; German.
XX CC The present invention provides a number of human immune system associated
XX CC genes which are modified by the methylation of cytosines. The sequences
XX CC can be used in the diagnosis and treatment of immune system disorders,
XX CC including eye diseases such as retinopathy, neovascular glaucoma and
XX CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
XX CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
XX CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
XX CC diseases. The present sequence is a gene of the invention.
XX SQ Sequence 6899 BP; 1802 A; 79 C; 1686 G; 3332 T; 0 other;

Query Match 11.6%; Score 31.8; DB 24; Length 6899;
Best Local Similarity 49.7%; Pred. NO. 9.5;
Matches 81; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

ov 87 agaagagaggttatccttcagggtggtaccagacagatgttctcaacttggttaaggag 146
1772 agaggtggaggttgtagtaagcagagattacgtttattttagtttggtataaagag 1831

Qy 147 gaagaaacccagtcgaatgaattcaatgaataattcttggaacttcacattgaagtgtag 206
1832 taagattcgattataaaaaaataaaataaaatgggtcggtggttaaatgttag 1891

Qy 207 attgagcaggtagtaattgcagtcagttgtgacattagtgcat 249
1892 agtgagtagtggtggtgaataggttttttttaagtat 1934

Db 1892 agtgagtagtggtggtgaataggttttttttaagtat 1934

RESULT 14
AAT65070
ID AAT65070 standard; DNA; 394 BP.
XX AC AAT65070;
XX DT 29-JAN-1998 (first entry)
XX DE Canine genomic microsatellite DNA.
XX KW canine; microsatellite; parentage testing; forensic test; breeding; dog;
XX KW PCR; LCR; primer; genotype; genetic diversity; polymorphism; ds.
XX OS Canis sp.
XX PH Key Location/Qualifiers
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/tag= a
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satellite 234..349
/tag= b
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misc_feature 350..394
/tag= c
/note= "unique flanking sequence"
XX PN WO9713876-A1.
XX PD 17-APR-1997.
XX PF 27-SEP-1996; 96WO-US15556.
XX PR 28-SEP-1995; 95US-0004469.
XX PA (PEZO-) PE ZOOGEN.
XX PI Dvorak J, Halverson J, Stevenson T;
XX WI 1997-235910/21.
XX PR Canine genotyping using micro-satellite length polymorphism - useful
```

```
PT for distinguishing individuals, testing of parentage and analysis of
PT relatedness
XX PS Claim 10; Page 26; 51pp; English.
XX CC This canine genomic DNA sequence has internal microsatellite repeats
XX CC that are flanked by unique flanking regions. The flanking sequences
XX CC uniquely identify the microsatellite locus within the genome. This is
XX CC used in a new method of genotyping a canine at a microsatellite locus,
XX CC where the chromosomal DNA comprising a repeated motif is amplified with
XX CC oligonucleotide primers specific for the locus and size fractionating
XX CC the product to measure chromosomal DNA size between the primers.
XX CC Information from multiple loci could be used for distinguishing
XX CC individuals, parentage testing and analysis of individuals' relatedness.
XX CC It is also useful in improving breeding programmes and population
XX CC diversity. A canine genome map could be constructed from analysis of
XX CC many loci for morphology, behaviour and disease studies and maximising
XX CC species genetic diversity.
XX SQ Sequence 394 BP; 96 A; 57 C; 47 G; 194 T; 0 other;

Query Match 11.6%; Score 31.6; DB 18; Length 394;
Best Local Similarity 55.5%; Pred. NO. 3.6;
Matches 61; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

Qy 147 gaagaaacccagtcgaatgaattcaatgaataattcttggaacttcacattgaagtgttag 206
73 gataaaacctgcctttgtaaatgaagaaatattgggtatatacttggatgaatgg 132

Qy 207 attgagcaggtagtaattgcagtcagttgtacattagtcattaaaaa 256
133 atggagaagaacctattttatgatttttaaaagttaggattatggga 182

Db 133 atggagaagaacctattttatgatttttaaaagttaggattatggga 182

RESULT 15
AAX17807
ID AAX17807 standard; DNA; 394 BP.
XX AC AAX17807;
XX DT 11-MAY-1999 (first entry)
XX DE Microsatellite repeat sequence from locus #7 of canine genotype.
XX KW Microsatellite repeat sequence; locus; canine; genotype; PCR; primer;
XX KW amplification; chromosome; polymorphism; parentage testing;
XX KW forensic testing; ds.
XX OS Canis familiaris.
XX PN US5874217-A.
XX PD 23-FEB-1999.
XX PF 27-MAR-1996; 96US-0623906.
XX PR 27-MAR-1996; 96US-0623906.
XX PA (PEKE ) PERKIN-ELMER CORP.
XX PI Dvorak J, Halverson J, Stevenson T;
XX WI 1999-179968/15.
XX PR Genotyping canines - by amplification of microsatellite DNA
XX PS Claim 10; Column 19-20; 27pp; English.
XX CC Sequences AAX17801-X17820 represent microsatellite repeat sequences from
XX CC loci of canine genotypes. The sequences can be used in a method for
XX CC genotyping a canine, by PCR amplifying a region of chromosomal DNA with
XX CC primers that specifically hybridise to a microsatellite locus, where the
```



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model  
Run on: August 16, 2002, 11:46:41 ; Search time 1853.82 Seconds  
(without alignments)  
3081.715 Million cell updates/sec

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Sequence: 1 ctaccacatctactccgacg.....agatgattattgattgctt 273

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb.ba.\*

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4: gb.om.\*

5: gb.ov.\*

6: gb.pat.\*

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8: gb.pl.\*

9: gb.pr.\*

10: gb.ro.\*

11: gb.sts.\*

12: gb.sy.\*

13: gb.un.\*

14: gb.vi.\*

15: em.ba.\*

16: em.fun.\*

17: em.in.\*

18: em.in.\*

19: em.mu.\*

20: em.om.\*

21: em.or.\*

22: em.ov.\*

23: em.pat.\*

24: em.ph.\*

25: em.pl.\*

26: em.ro.\*

27: em.sts.\*

28: em.un.\*

29: em.vi.\*

30: em.htg\_hum.\*

31: em.htg\_inv.\*

32: em.htg\_other.\*

33: em.htgo\_inv.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Score Match Length DB ID Description

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2	273	100.0	1410	9	HUMPYDH
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4	273	100.0	1446	9	HUMPDH1B
5	273	100.0	1472	6	AX151747
6	273	100.0	1472	9	HUMPDH1A
7	273	100.0	17072	9	HUMPDHAL
8	273	100.0	195191	2	AC025563
9	270	98.9	1427	9	HSPDHBE1
10	270	98.9	1456	9	HSPDHBE1
11	268.2	98.2	1492	9	HSPDHBE1
12	267	97.8	1417	9	HSPDHBE1
13	194	71.1	201	11	G13505
14	115	42.1	129	9	S57358
15	90	33.0	149	9	S81593
16	69	25.3	2854	10	RRPDH1A
17	67.4	24.7	1446	10	MUSPDH1A
18	67.4	24.7	2778	10	BC007142
19	67.4	24.7	158565	2	AC106221
20	65.4	24.0	3055	9	HUMPYRDH
21	65.4	24.0	111547	2	AP002332
22	65.4	24.0	146072	9	AC093828
23	63.6	23.3	1344	4	SNPDHA
24	63	23.1	1170	4	SDPDH1A
25	49	17.9	67	9	S56181
26	47.8	17.5	2349	10	MUSPDHA2A
27	47.8	17.5	58040	2	AC101628
28	47.8	17.5	211301	2	AC100752
29	46	16.8	1616	10	RRPDH1A2
30	46	16.8	2228	10	RNU4125
31	42.2	15.5	154854	2	AC015539
32	42.2	15.5	171589	2	AC073567
33	42.2	15.5	175466	2	AC016419
34	39.8	14.6	163794	2	AC103449
35	39.4	14.4	157511	9	AC074348
36	38.6	14.1	145269	2	AC096563
37	38.4	14.1	168662	9	AC079880
38	38.4	14.1	186343	9	AL137248
39	38.4	14.1	196966	2	AC031975
40	38.2	14.0	39002	9	AF001219
41	38.2	14.0	39494	9	AF001217
42	38.2	14.0	39946	9	AF001220
43	38.2	14.0	109101	2	AC108674
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RESULT 1

HUMPDHA12

LOCUS

DEFINITION

Human nuclear-encoded mitochondrial pyruvate dehydrogenase E1 alpha

(pdhE1-a) subunit gene, exon 11.

ACCESSION

VERSION

KEYWORDS

SEGMENT

SOURCE

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

REFERENCE

367 bp DNA linear PRI 08-JAN-1995  
Human nuclear-encoded mitochondrial pyruvate dehydrogenase E1 alpha  
(pdhE1-a) subunit gene, exon 11.

M27257 J02734 M27166

M27257.1 GI:488487

dehydrogenase; nuclear-encoded mitochondrial EF-G-like protein;

pyruvate dehydrogenase.

12 of 12

Human fetal liver, cDNA to mRNA, clones lambda-PDH[1,5,7 and F];

and leukocyte DNA, clones cpDH[3,4a].

Homo sapiens

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 9 to 367)

Dahl, H.H., Hunt, S.M., Hutchison, W.M. and Brown, G.K.

The human pyruvate dehydrogenase complex. Isolation of cDNA clones

for the E1 alpha subunit, sequence analysis, and characterization

of the mRNA

J. Biol. Chem. 262 (15), 7398-7403 (1987)

8722349

2 (bases 1 to 14; 168 to 173)



AUTHORS Maragos,C., Hutchison,W.M., Hayasaka,K., Brown,G.K. and Dahl,H.H.  
 TITLE Structural organization of the gene for the E1 alpha subunit of the human pyruvate dehydrogenase complex  
 JOURNAL J. Biol. Chem. 264 (21), 12294-12298 (1989)  
 MEDLINE 89308653  
 COMMENT On May 21, 1994 this sequence version replaced gi:189750.  
 Draft entry and computer-readable sequence of [1] kindly provided by H.-H.M.Dahl, 10-APR-1987.

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 99 t

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Query Match 100.0%; Score 273; DB 9; Length 367;  
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 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 95 CTACCACATCTACTCCAGCGACCCACCTTTTGAAGTTCGTGGTGCATATCAGTGATCAA 154

Qy 61 gtttaagtcagtcagtttaaggaggagagagaggttatcaccttcaggggggtaccac 120  
 Db 155 GTTTAAGTCAGTCAGTTAAGGGAGGAGAGAGAGGTTATACCTTCAGGGGGGTACCAG 214

Qy 121 acagtgttctcaacttgggttaaggaggagaaaacccagtcagtaattcaatgaatt 180

Db 215 ACAGTGTCACAACTTGGTTAAGGAGGAGAAACCCAGTCAATGAAATTCGAATTAATT 274  
 Qy 181 cttggaactccattaaagtgtgtagattgagcagtagtagtaattgcagtcagttgtaca 240  
 Db 275 CTTGGAACACTTCCATTAAAGTGTGTAGATTGAGCAGGTAGTAGTAATTCATGCATGTCAC 334  
 Qy 241 ttagtcattaaagatgaattatttgagtgctt 273  
 Db 335 TTAGTCATTAAAGATGAATTTATTGAGTGCTT 367

RESULT 2  
 LOCUS HUMPYDH  
 DEFINITION Human pyruvate dehydrogenase alpha subunit mRNA linear PRI 27-APR-1993  
 ACCESSION M24848  
 VERSION M24848.1 GI:190761  
 KEYWORDS pyruvate dehydrogenase alpha subunit.  
 SOURCE Human liver, cDNA to mRNA.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 AUTHORS Ho,L., Wexler,I.D., Liu,T.-C., Thekkumkara,T.J. and Patel,M.S.  
 TITLE Characterization of cDNAs encoding human pyruvate dehydrogenase  
 alpha-subunit  
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 86, 5330-5334 (1989)  
 MEDLINE 89315791  
 COMMENT Draft entry and computer-readable sequence for [1] kindly submitted  
 by M.S.Patel, 16-MAY-1989  
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 373 a 296 c 402 g 339 t  
 BASE COUNT  
 ORIGIN Unreported.

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 Best Local Similarity 100.0%; Pred. No. 2e-66;  
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ctaccacatctactccagcgaccaccccttttgagttcgttggtgccaatcagtgatcaaa 60  
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Qy 61 gtttaagtcagtcagtttaaggaggagagagaggttatcaccttcaggggggtaccac 120  
 Db 1198 GTTTAAGTCAGTCAGTTAAGGGAGGAGAGAGAGGTTATACCTTCAGGGGGGTACCAG 1257

Qy 121 acagtgttctcaacttgggttaaggaggagaaaacccagtcagtaattcaatgaatt 180  
 Db 1258 ACAGTGTCTCAACTTGGTTAAGGAGGAGAAACCCAGTCAATGAAATTCGAATTAATT 1317

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QY 181 cttggaactccattgaagtgttagatgagcagtaagtaattgcatgcaattgtatca 240
Db 1318 CTTGGAACCTTCATTAAGTGTGTAGATTGAGCAGTAGTAATTGTCAGTTGTGACA 1377
QY 241 ttatgtcattaaagatgaattattgagtgctt 273
Db 1378 TTATGTCATTAAGATGAATTATGATGCTT 1410

RESULT 3
LOCUS HUMPDHA 1419 bp mRNA linear PRI 07-JAN-1995
DEFINITION Human pyruvate dehydrogenase alpha subunit mRNA, complete cds.
ACCESSION J03575
VERSION J03575.1 GI:189737
KEYWORDS pyruvate dehydrogenase.
SOURCE Human foreskin fibroblast, cDNA to mRNA, clone PHPDA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1419)
Koike,K., Ohta,S., Urata,Y., Kagawa,Y. and Koike,M.
Cloning and sequencing of cDNAs encoding alpha and beta subunits of
human pyruvate dehydrogenase
Proc. Natl. Acad. Sci. U.S.A. 85 (1), 41-45 (1988)
88124815
2 (bases 1 to 1419)
Koike,K., Urata,Y., Matsuo,S. and Koike,M.
Characterization and nucleotide sequence of human pyruvate
dehydrogenase alpha subunit gene
Unpublished (1990)
[2] revises [1].
Draft entry and printed copy of sequence for [1] kindly provided by
K.Koike, 11-APR-1988; and computer-readable copy for [2],
12-MAR-1990.

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    YGGNGVQPLGALACKYNGKDEVLTYLGDGAANQGOIFEAYNNKALMKLPC
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sig_peptide
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BASE COUNT 377 a 297 c 403 g 342 t
ORIGIN

Query Match 100.0%; Score 273; DB 9; Length 1419;
Best Local Similarity 100.0%; Pred. No. 2e-66; 0; Gaps 0;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctaccacatctactccagcaccacaccttttgagctgtggtgagccaatcagtgatcaa 60

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Db 1140 CTACCACATCTACTCCAGGACCCACCTTTTGAAGTTCGTGGTGCCAAATCAGTGAACAA 1199
QY 61 gtttaagtcaagtaagggaggaggaaggaggttatacccttcaggggggtaccag 120
Db 1200 GTTTAAGTCAGTCAGTTAAGGGGAGGAGAGAGGTTTACCTTCAGGGGGGTACCAG 1259
QY 121 acagtgcttcaactggttaaggaggaagaaacccagcgaatgaatcaatgaatt 180
Db 1260 ACAGTGTCTCAACTTGGTTAAGGAGGAGAAACCCAGTCATGAATTCATGAATTT 1319
QY 181 cttggaactccattgaagtgttagatgagcaggtagtaattgcatgcaattgttaca 240
Db 1320 CTTGGAACCTTCATTAAGTGTGTAGATTGAGCAGTAGTAATTGTCAGTTGTGACA 1379
QY 241 ttatgtcattaaagatgaattattgagtgctt 273
Db 1380 TTATGTCATTAAGATGAATTATGATGCTT 1412

RESULT 4
LOCUS HUMPDHELB 1446 bp mRNA linear PRI 07-JAN-1995
DEFINITION Human pyruvate dehydrogenase E1-alpha subunit mRNA, cds.
ACCESSION J03503
VERSION J03503.1 GI:189765
KEYWORDS pyruvate dehydrogenase.
SOURCE Human hepatoma, cDNA to mRNA, clone lambda-gt11.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1446)
De Weirleir,L., Mackay,N., Lam Hon Wah,A.M. and Robinson,B.H.
Isolation of a full-length complementary DNA coding for human E1
alpha subunit of the pyruvate dehydrogenase complex
J. Biol. Chem. 263 (4), 1991-1995 (1988)
88115327
COMMENT Clean copy of sequence [1] kindly provided by B.Robinson
(03/08/88).

FEATURES
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    ELTGKGCAGKGGSGMMIAKNFYGGNGVQPLGALACKYNGKDEVLTYLGDGAANQGOI
    FEAYNNKALMKLPCIFICENNRGMGTSPVRAAATDYIKRGDFIPLGRVDGMDILCVRE
    ATFRAAAYCRSGKGPILMELQTYRHHGMSDPGVSYTRREIQVRSKSDPILMLKDMVNS
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    379 a 307 c 414 g 346 t

BASE COUNT 379 a 307 c 414 g 346 t
ORIGIN 128 bp upstream of NaeI site.

Query Match 100.0%; Score 273; DB 9; Length 1446;
Best Local Similarity 100.0%; Pred. No. 2e-66; 0; Gaps 0;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	gtttaagtccaagtcagtttaaggggagagaagagattatcaccttcagggggctaccag	120
Db	1227	GTTTAAGTCAGTCAGTTAAGGGGAGGAGAGAGATTATACCTTCAGGGGGCTACCAG	1286
Qy	121	acagtggtctcaacttggttaaggagagaagaaacccagtcgaatgaaattcaatgaaatt	180
Db	1287	ACAGTGTCTCAACTTGGTTAAGGAGGAAGAAAACCCAGTCAAATGAAATTCAAATGAAAT	1346
Qy	181	cttggaaactcccattaaagtgttagattgaagcaggttagtaattgcacagtttgtaca	240
Db	1347	CTTGGAAACTTCCAATTAAGTGTGTAGATTGACGAGGTAGTAATTGCATGCAGTTGTGACA	1406
Qy	241	ttagtgcattaaaagatgaattattgagtgcct	273
Db	1407	TTAGTGCATTAAAAAGATGAATATTAGTGCTT	1439
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AXI51747			
LOCUS	AXI51747	1472 bp	DNA linear PAT 22-JUN-2001
DEFINITION	Sequence 2 from Patent EP1118680.		
ACCESSION	AXI51747		
VERSION	AXI51747.1 GI:14533675		
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Smith,J.C., Anand,R.A. and Morten,J.E.		
TITLE	Method for the diagnosis of polymorphisms in the human pdh elalpha gene		
JOURNAL	Patent: EP 1118680-A 2 25-JUL-2001;		
FEATURES	Astrazeneca AB (SE) Location/Qualifiers 1..1472 /organism="Homo sapiens" /db_xref="taxon:9606"		
BASE COUNT	381 a	314 c	427 g 350 t
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atches 273;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
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Qy	61	gtttaagtccaagtcagtttaaggggagagaagagattatcaccttcagggggctaccag	120
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Db	1320	ACAGTGTCTCAACTTGGTTAAGGAGGAAGAAAACCCAGTCAAATGAAATTCAAATGAAAT	1379
Qy	181	cttggaaactcccattaaagtgttagattgaagcaggttagtaattgcacagtttgtaca	240
Db	1380	CTTGGAAACTTCCAATTAAGTGTGTAGATTGACGAGGTAGTAATTGCATGCAGTTGTGACA	1439
Qy	241	ttagtgcattaaaagatgaattattgagtgcct	273
Db	1440	TTAGTGCATTAAAAAGATGAATATTAGTGCTT	1472

**RESULT 6**

HUMPUDE1A	1472 bp	mrna	linear	PRI 08-JAN-1999
LOCUS	Human pyruvate dehydrogenase E1-alpha subunit (PDHA1) mRNA, complete cds.			
DEFINITION	L13318 J02734			
ACCESSION	L13318.1 GI:292412			
VERSION	pyruvate dehydrogenase			
KEYWORDS	pyruvate dehydrogenase; pyruvate dehydrogenase E1-alpha subunit.			
SOURCE	Homo sapiens fetus and adult liver cDNA to mRNA.			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
AUTHORS	1 (bases 1 to 1472)			
TITLE	Dahl,H.H., Hunt,S.M., Hutchison,W.M. and Brown,G.K. The human pyruvate dehydrogenase complex. Isolation of cDNA clones for the E1 alpha subunit, sequence analysis, and characterization of the mRNA			
JOURNAL	J. Biol. Chem. 262 (15), 7398-7403 (1987)			
MEDLINE	87223349			
REFERENCE	2 (sites)			
AUTHORS	Maragos,C., Hutchison,W.M., Hayasaka,K., Brown,G.K. and Dahl,H.H. Structural organization of the gene for the E1 alpha subunit of the human pyruvate dehydrogenase complex			
TITLE	J. Biol. Chem. 264 (21), 12294-12298 (1989)			
JOURNAL	89308653			
MEDLINE				
FEATURES	Location/Qualifiers			
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5'UTR	1..105			
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	1447..1452			
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ORIGIN				

**RESULT 6**

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Best Local Similarity 100.0%; Pred.No. 2e-66;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ctaccacatctactccagcaccacaccttttgagtgtggtgcgaatcaatgatcaa 60
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Db - 1200 CTACCACATCTACTCCAGCACCACCTTTTGAAGTTCGTGCGCAATCATGGATCAA 1259
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QY      61 gtttaagtcoagtcagttaaggaggagaaggagattataccttcagggggctaccag 120
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Db 1260 GTTTAAGTCAGTCAGTTAAAGGGAGGAGAAGGAGGTTTATACCTTCAGGGGCTACCAG 1319
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QY      121 acagtttctcaacttggttaaggaggagaagaaacccagtcgaatgaattcaatgaaatt 180
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Db 1320 ACAGTGTCTCACTGGTTAAGGAGGAAGAACCCAGTCAATGAANTTCAATGAATT 1379
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QY      181 cttggaaaacttcattaagtgtgtagttgagcaggtagtaattgcagtttgtaca 240
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Db 1380 CTTGGAACCTTCATTAAAGTGTTAGTAGTGCAGGAGTAGTAATTCATCGAGCTTTGTACA 1439
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Db 241 ttagtcatataaagatgaattattgagtgctt 273
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Db 1440 TTAGTGCATTAAAAGATGAATTATTGAGTGCTT 1472
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RESULT       7
HUMPDHAL
LOCUS        HUMPDHAL               17072 bp    DNA          linear   PRI 01-FEB-2000
DEFINITION   Human pyruvate dehydrogenase [EC 1.2.4.1] alpha subunit gene, exons
              1-11.
ACCESSION    D90084 M58568
VERSION      D90084.1 GI:219981
KEYWORDS     pyruvate dehydrogenase; pyruvate dehydrogenase alpha subunit.
SOURCE       Human leukocyte DNA, clones pGPdHA[13 and 37].
ORGANISM     Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 17072)
AUTHORS      Koike,K., Urata,Y., Matsuo,S. and Koike,M.
TITLE        Characterization and nucleotide sequence of the gene encoding the
              human pyruvate dehydrogenase alpha-subunit
JOURNAL       Gene 93 (2), 307-311 (1990)
MEDLINE      91033044
COMMENT      These data kindly submitted in computer readable form by: Kichiko
              Koike
              Department of Pathological Biochemistry
              Atomic Disease Institute Nagasaki University School of Medicine
              12-4, Sakamoto-machi
              Nagasaki-shi 852
              Japan
              Phone: 0958-47-2111
              Fax: 0958-47-8514
              First 10 bp reported in [1] is linker sequence.
FEATURES     Location/Qualifiers
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protein_bind 370..375
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TATA_signal 429..434
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exon         439..619
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CODS         10908..11000,11767..11922,12107..12178,14064..14131,
              15318..15426,15888..16052)
              /note="alpha subunit"
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Mon Aug 19 09:13:23 2002

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/db_xref="GI:12803199"
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YGGNIVGAQVPLGATACCKYNGDEVLTLVGDGAANOQOIFRAYNAAALWKLPC
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BASE COUNT      408 a 302 c 406 g 340 t
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Query Match      98.9%; Score 270; DB 9; Length 1456;
Best Local Similarity 100.0%; Pred. No. 1.4e-65;
Matches 270; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ctaccacatctactccagcacccttttgaagtctggtggtgccaatcagtgatcaa 60
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QY 61 gtttaagtcagtcagtaaggggagagagagagagagagagagagagagagagag 120
DB 1212 GTTTAAGTCAGTCAGTTAAGGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1271
QY 121 acagtgcttcaactggttaagggagagagagagagagagagagagagagagag 180
DB 1272 ACAGTGTCTCACTGTTAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1331
QY 181 cttggaacttcattgaagtgtagatgagcagagagagagagagagagagagag 240
DB 1332 CTTGGAACCTTCCATTGAAGTGTAGATGAGCAGGTAGTAAATGCAATGATGATA 1391
QY 241 ttatgcattaaaagatgaattattgagtg 270
DB 1392 TTATGCAATTAAGATGAATTAATTGAGTG 1421

RESULT 11
HUMPDHALG      1492 bp      mRNA      linear      PRI 15-AUG-2000
LOCUS          Homo sapiens pyruvate dehydrogenase E1-alpha subunit precursor
DEFINITION     (PDHAL) mRNA, complete cds.
ACCESSION      L48690
VERSION        L48690.1 GI:1051096
KEYWORDS       human.
SOURCE         Homo sapiens
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE      1 (bases 1 to 1492)
AUTHORS        Dahl, H.H., Brown, G.K., Brown, R.M., Hansen, L.L., Kerr, D.S.,
               Mackay, I.D., Patel, M.S., De Meirleir, L., Lissens, W., Chun, K.,
               Mackay, N. and Robinson, B.H.
               Mutations and polymorphisms in the pyruvate dehydrogenase E1 alpha
               gene
               Hum. Mutat. 1 (2), 97-102 (1992)
JOURNAL        93244853
MEDLINE        1301207
PUBMED         2 (bases 1 to 1492)
REFERENCE      Takakubo, F., Cartwright, P., Hoogenraad, N., Thorburn, D.R.,
               Collins, F., Lithgow, T. and Dahl, H.H.
               An amino acid substitution in the pyruvate dehydrogenase E1 alpha
               gene, affecting mitochondrial import of the precursor protein
               Am. J. Hum. Genet. 57 (4), 772-780 (1995)
JOURNAL        96029268
MEDLINE

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Best Local Similarity 100.0%; Pred. No. 1.4e-65;
Matches 270; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 10
BC002406      1456 bp      mRNA      linear      PRI 12-JUL-2001
LOCUS          Homo sapiens, pyruvate dehydrogenase (lipoamide) alpha 1, clone
DEFINITION     MGC:8609 IMAGE:2961286, mRNA, complete cds.
ACCESSION      BC002406
VERSION        BC002406.1 GI:12803198
KEYWORDS       MGC.
SOURCE         human.
ORGANISM       Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
               1 (bases 1 to 1456)
               Strausberg, R.
Direct Submission
Submitted (05-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgabs@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nih.gov
Shcherbenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Masello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Stantripop, S., Thomas, P.J.,
Tiongson, E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 1 Row: 1 Column: 24
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4505684.
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human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 1417)  
Song, B.J.  
Direct Submission  
Submitted (18-APR-1990) Song B.J., National Institute on Alcohol  
Abuse and Alcoholism, Laboratory of Metabolism and Molecular  
Biology, 12501 Washington Ave., Rockville, MD 20852, USA  
2 (bases 1 to 1417)  
Huh, T.L., Chi, Y.T., Casazza, J.P., Veech, R.L. and Song, B.J.  
Unpublished  
Data kindly reviewed (05-NOV-1990) by Song B.J.  
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DB 1331 CTGGAAACTTCCACTTGAAGGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1390  
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HSPDHLE1  
LOCUS Human mRNA for liver pyruvate dehydrogenase (EC 1.2.4.1) E1'  
DEFINITION subunit.  
ACCESSION X52710  
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